



SEQUENCE LISTING

RECEIVED

JUN 26 2001

TECH CENTER 1600/2900

<110> MURDIN, ANDREW D.  
OOMEN, RAYMOND P.  
WANG, JOE  
DUNN, PAMELA

<120> CHLAMYDIA ANTIGENS AND CORRESPONDING  
DNA FRAGMENTS AND USES THEREOF

<130> 032931/0227

<140> 09/523,647

<141> 2000-03-10

<150> 60/123,966

<151> 1999-03-12

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 2111

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (139)..(1809)

<400> 1

```
ttgatcaggt agttaggaga tgaattaatt cctgactacc ttaattcaga taataaaccc 60
aaatgttgag ggtaagagtt tacaaaaacat tctacccgat ggcagaagaa aaaaataaac 120
atgcgatagg agatccct atg tcc aaa ctc atc aga cga gta gtt acg gtc 171
          Met Ser Lys Leu Ile Arg Arg Val Val Thr Val
          1              5              10
ctt gcg cta acg agt atg gcg agt tgc ttt gcc agc ggg ggt ata gag 219
Leu Ala Leu Thr Ser Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu
          15              20              25
gcc gct gta gca gag tct ctg att act aag atc gtc gct agt gcg gaa 267
Ala Ala Val Ala Glu Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu
          30              35              40
aca aag cca gca cct gtt cct atg aca gcg aag aag gtt aga ctt gtc 315
Thr Lys Pro Ala Pro Val Pro Met Thr Ala Lys Lys Val Arg Leu Val
          45              50              55
cgt aga aat aaa caa cca gtt gaa caa aaa agc cgt ggt gct ttt tgt 363
Arg Arg Asn Lys Gln Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys
          60              65              70              75
```

gat aaa gaa ttt tat ccc tgt gaa gag gga cga tgt caa cct gta gag	411
Asp Lys Glu Phe Tyr Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu	
80 85 90	
gct cag caa gag tct tgc tac gga aga ttg tat tct gta aaa gta aac	459
Ala Gln Gln Glu Ser Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn	
95 100 105	
gat gat tgc aac gta gaa att tgc cag tcc gtt cca gaa tac gct act	507
Asp Asp Cys Asn Val Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr	
110 115 120	
gta gga tct cct tac cct att gaa atc ctt gct ata ggc aaa aaa gat	555
Val Gly Ser Pro Tyr Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp	
125 130 135	
tgt gtt gat gtt gtg att aca caa cag cta cct tgc gaa gct gaa ttc	603
Cys Val Asp Val Val Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe	
140 145 150 155	
gta agc agt gat cca gaa aca act cct aca agt gat ggg aaa tta gtc	651
Val Ser Ser Asp Pro Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val	
160 165 170	
tgg aaa atc gat cgc ctg ggt gca gga gat aaa tgc aaa att act gta	699
Trp Lys Ile Asp Arg Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val	
175 180 185	
tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttc aca gct gct act gta	747
Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val	
190 195 200	
tgt gct tgc cca gag ctc cgt tct tat act aaa tgc ggt caa cca gcc	795
Cys Ala Cys Pro Glu Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala	
205 210 215	
att tgt att aag caa gaa gga cct gac tgt gct tgc cta aga tgc cct	843
Ile Cys Ile Lys Gln Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro	
220 225 230 235	
gta tgc tac aaa atc gaa gta gtg aac aca gga tct gct att gcc cgt	891
Val Cys Tyr Lys Ile Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg	
240 245 250	
aac gta act gta gat aat cct gtt ccc gat ggc tat tct cat gca tct	939
Asn Val Thr Val Asp Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser	
255 260 265	
ggg caa aga gtt ctc tct ttt aac tta gga gac atg aga cct ggc gat	987
Gly Gln Arg Val Leu Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp	
270 275 280	
aaa aag gta ttt aca gtt gag ttc tgc cct caa aga aga ggt caa atc	1035
Lys Lys Val Phe Thr Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile	
285 290 295	

---

act aac gtt gct act gta act tac tgc ggt gga cac aaa tgt tct gca	1083
Thr Asn Val Ala Thr Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala	
300 305 310 315	
aat gta act aca gtt gtt aat gag cct tgt gta caa gta aat atc tct	1131
Asn Val Thr Thr Val Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser	
320 325 330	
ggt gct gat tgg tct tac gta tgt aaa cct gtg gag tac tct atc tca	1179
Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser	
335 340 345	
gta tcg aat cct gga gac ttg gtt ctt cat gat gtc gtg atc caa gat	1227
Val Ser Asn Pro Gly Asp Leu Val Leu His Asp Val Val Ile Gln Asp	
350 355 360	
aca ctc cct tct ggt gtt aca gta ctc gaa gct cct ggt gga gag atc	1275
Thr Leu Pro Ser Gly Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile	
365 370 375	
tgc tgt aat aaa gtt gtt tgg cgt att aaa gaa atg tgc cca gga gaa	1323
Cys Cys Asn Lys Val Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu	
380 385 390 395	
acc ctc cag ttt aaa ctt gta gtg aaa gct caa gtt cct gga aga ttc	1371
Thr Leu Gln Phe Lys Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe	
400 405 410	
aca aat caa gtt gca gta act agt gag tct aac tgc gga aca tgt aca	1419
Thr Asn Gln Val Ala Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr	
415 420 425	
tct tgc gca gaa aca aca aca cat tgg aaa ggt ctt gca gct acc cat	1467
Ser Cys Ala Glu Thr Thr Thr His Trp Lys Gly Leu Ala Ala Thr His	
430 435 440	
atg tgc gta tta gac aca aat gat cct atc tgt gta gga gaa aat act	1515
Met Cys Val Leu Asp Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr	
445 450 455	
gtc tat cgt atc tgt gta act aac cgt ggt tct gct gaa gat act aac	1563
Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn	
460 465 470 475	
gta tct tta atc ttg aag ttc tca aaa gaa ctt cag cca ata gct tct	1611
Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser	
480 485 490	
tca ggt cca act aaa gga acg att tca ggt aat acc gtt gtt ttc gac	1659
Ser Gly Pro Thr Lys Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp	
495 500 505	
gct tta cct aaa ctc ggt tct aag gaa tct gta gag ttt tct gtt acc	1707
Ala Leu Pro Lys Leu Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr	
510 515 520	

---

ttg aaa ggt att gct ccc gga gat gct cgc ggc gaa gct att ctt tct 1755  
 Leu Lys Gly Ile Ala Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser  
 525 530 535

tct gat aca ctg act tca cca gta tca gac aca gaa aat acc cac gtg 1803  
 Ser Asp Thr Leu Thr Ser Pro Val Ser Asp Thr Glu Asn Thr His Val  
 540 545 550 555

tat taa attctaagga attatcctaa agcagagcga tattccgctc tgcttttagga 1859  
 Tyr

tagctttcaa agaagtaccg ctttagtacc ttacgtacta aagcgggtttt tttgttttat 1919  
 aagctctttca atccaatcgt agagtttctt aatcaaagat attattttaag tttctgaaat 1979  
 cctaagattt attttaaaag cccatctttt taggtatgta attaaaattt ttaattaagc 2039  
 ttttcttagt gtaacctgct tcttttaggaa ctacactagg agaacggat gtcacaaat 2099  
 ctacatcccg ta 2111

<210> 2  
 <211> 556  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 2  
 Met Ser Lys Leu Ile Arg Arg Val Val Thr Val Leu Ala Leu Thr Ser  
 1 5 10 15  
 Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu Ala Ala Val Ala Glu  
 20 25 30  
 Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu Thr Lys Pro Ala Pro  
 35 40 45  
 Val Pro Met Thr Ala Lys Lys Val Arg Leu Val Arg Arg Asn Lys Gln  
 50 55 60  
 Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys Asp Lys Glu Phe Tyr  
 65 70 75 80  
 Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu Ala Gln Gln Glu Ser  
 85 90 95  
 Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn Asp Asp Cys Asn Val  
 100 105 110  
 Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr  
 115 120 125  
 Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp Cys Val Asp Val Val  
 130 135 140  
 Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro  
 145 150 155 160

Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val Trp Lys Ile Asp Arg  
 165 170 175  
 Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu  
 180 185 190  
 Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu  
 195 200 205  
 Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala Ile Cys Ile Lys Gln  
 210 215 220  
 Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro Val Cys Tyr Lys Ile  
 225 230 235 240  
 Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg Asn Val Thr Val Asp  
 245 250 255  
 Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser Gly Gln Arg Val Leu  
 260 265 270  
 Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp Lys Lys Val Phe Thr  
 275 280 285  
 Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile Thr Asn Val Ala Thr  
 290 295 300  
 Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala Asn Val Thr Thr Val  
 305 310 315 320  
 Val Asn Glu Pro Cys Val Gln Val Asn Ile Ser Gly Ala Asp Trp Ser  
 325 330 335  
 Tyr Val Cys Lys Pro Val Glu Tyr Ser Ile Ser Val Ser Asn Pro Gly  
 340 345 350  
 Asp Leu Val Leu His Asp Val Val Ile Gln Asp Thr Leu Pro Ser Gly  
 355 360 365  
 Val Thr Val Leu Glu Ala Pro Gly Gly Glu Ile Cys Cys Asn Lys Val  
 370 375 380  
 Val Trp Arg Ile Lys Glu Met Cys Pro Gly Glu Thr Leu Gln Phe Lys  
 385 390 395 400  
 Leu Val Val Lys Ala Gln Val Pro Gly Arg Phe Thr Asn Gln Val Ala  
 405 410 415  
 Val Thr Ser Glu Ser Asn Cys Gly Thr Cys Thr Ser Cys Ala Glu Thr  
 420 425 430  
 Thr Thr His Trp Lys Gly Leu Ala Ala Thr His Met Cys Val Leu Asp  
 435 440 445  
 Thr Asn Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys  
 450 455 460

---

Val Thr Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu  
 465 470 475 480

Lys Phe Ser Lys Glu Leu Gln Pro Ile Ala Ser Ser Gly Pro Thr Lys  
 485 490 495

Gly Thr Ile Ser Gly Asn Thr Val Val Phe Asp Ala Leu Pro Lys Leu  
 500 505 510

Gly Ser Lys Glu Ser Val Glu Phe Ser Val Thr Leu Lys Gly Ile Ala  
 515 520 525

Pro Gly Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr  
 530 535 540

Ser Pro Val Ser Asp Thr Glu Asn Thr His Val Tyr  
 545 550 555

<210> 3

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

ataagaatgc ggccgccacc atgtccaaac tcatcagacg agtag 45

<210> 4

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

gcgccggatc cgatacacgt gggatattttc tgtg 34